

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=18; hr=18; min=38; sec=30; ms=789;
]

=====

Application No: 10590464

Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-21 19:04:04.576

Finished: 2008-10-21 19:04:06.187

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 611 ms

Total Warnings: 25

Total Errors: 0

No. of SeqIDs Defined: 29

Actual SeqID Count: 29

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)

Input Set:

Output Set:

Started: 2008-10-21 19:04:04.576
Finished: 2008-10-21 19:04:06.187
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 611 ms
Total Warnings: 25
Total Errors: 0
No. of SeqIDs Defined: 29
Actual SeqID Count: 29

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences
City of Yokohama

<120> TRF2 DNA-binding domain mutant proteins, telomeric DNA mutants, and use of a
structure of a complex between a TRF2 DNA binding domain and a double-stranded DNA molecule

<130> FP-047PCT

<140> 10590464

<141> 2008-10-21

<150> JP P2004-046238

<151> 2004-02-23

<160> 29

<170> PatentIn version 3.1

<210> 1

<211> 189

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(189)

<400> 1

gaa gac agt aca acc aat ata aca aaa aag cag aag tgg act gta gaa	48
Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu	
1 5 10 15	

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg	144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val	
35 40 45	

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac	189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn	
50 55 60	

<210> 2

<211> 63

<212> PRT

<213> Homo sapiens

<400> 2

Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu

1	5	10	15
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn			
20	25	30	
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val			
35	40	45	
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn			
50	55	60	

<210> 3
 <211> 189
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic DNA

<220>
 <221> CDS
 <222> (1)..(189)
 <223> Mutant K447R of hTRF2-DBD

<400> 3	
gaa gac agt aca acc aat ata aca aaa agg cag aag tgg act gta gaa	48
Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu	
1 5 10 15	
gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	
tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg	144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val	
35 40 45	
atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac	189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn	
50 55 60	

<210> 4
 <211> 63
 <212> PRT
 <213> Artificial

<220>
 <223> Mutant K447R of hTRF2-DBD

<400> 4

Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu

1	5	10	15
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn			
20	25	30	
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val			
35	40	45	
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn			
50	55	60	

<210> 5
 <211> 189
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic DNA

<220>
 <221> CDS
 <222> (1)..(189)
 <223> Mutant A471S of hTRF2-DBD

<400> 5	
gaa gac agt aca acc aat ata aca aaa aag cag aag tgg act gta gaa	48
Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu	
1 5 10 15	
gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	
tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg	144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val	
35 40 45	
atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac	189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn	
50 55 60	

<210> 6
 <211> 63
 <212> PRT
 <213> Artificial

<220>
 <223> Mutant A471S of hTRF2-DBD

<400> 6

Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu

1	5	10	15
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn			
20	25	30	

Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
50 55 60

<210> 7
 <211> 189
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic DNA

<220>
 <221> CDS
 <222> (1)..(189)
 <223> Mutant A484S of hTRF2-DBD

<400> 7	
gaa gac agt aca acc aat ata aca aaa aag cag aag tgg act gta gaa	48
Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu	
1 5 10 15	

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg	144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val	
35 40 45	

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac	189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn	
50 55 60	

<210> 8
 <211> 63
 <212> PRT
 <213> Artificial

<220>
 <223> Mutant A484S of hTRF2-DBD

<400> 8

Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu

1	5	10	15
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn			
20	25	30	
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val			
35	40	45	
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn			
50	55	60	

<210> 9
 <211> 189
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic DNA

<220>
 <221> CDS
 <222> (1)..(189)
 <223> Mutant R496K of hTRF2-DBD

<400> 9	
gaa gac agt aca acc aat ata aca aaa aag cag aag tgg act gta gaa	48
Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu	
1 5 10 15	
gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	
tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg	144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val	
35 40 45	
atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac	189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn	
50 55 60	

<210> 10
 <211> 63
 <212> PRT
 <213> Artificial

<220>
 <223> Mutant R496K of hTRF2-DBD

<400> 10

Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu

1	5	10	15
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn			
20	25	30	

Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
50 55 60

<210> 11
 <211> 189
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic DNA

<220>
 <221> CDS
 <222> (1)..(189)
 <223> Mutant qm of hTRF2-DBD

<400> 11	
gaa gac agt aca acc aat ata aca aaa agg cag aag tgg act gta gaa	48
Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu	
1 5 10 15	

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg	144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val	
35 40 45	

atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac	189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn	
50 55 60	

<210> 12
 <211> 63
 <212> PRT
 <213> Artificial

<220>
 <223> Mutant qm of hTRF2-DBD

<400> 12

Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu

1	5	10	15
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn			
20	25	30	
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val			
35	40	45	
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn			
50	55	60	

<210> 13
 <211> 189
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic DNA

<220>
 <221> CDS
 <222> (1)..(189)
 <223> Mutant dm of hTRF2-DBD

<400> 13	
gaa gac agt aca acc aat ata aca aaa aag cag aag tgg act gta gaa	48
Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu	
1 5 10 15	
gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	
tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg	144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val	
35 40 45	
atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac	189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn	
50 55 60	

<210> 14
 <211> 63
 <212> PRT
 <213> Artificial

<220>
 <223> Mutant dm of hTRF2-DBD

<400> 14

Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu

1	5	10	15
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn			
20	25	30	
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val			
35	40	45	
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn			
50	55	60	

<210> 15
 <211> 1500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1500)

<400> 15	
atg gcg gga gga ggc ggg agt agc gac ggc agc ggg cgg gca gct ggc	48
Met Ala Gly Gly Gly Gly Ser Ser Asp Gly Ser Gly Arg Ala Ala Gly	
1 5 10 15	
agg cgg gcg tcc cgc agt agc ggg cgg gcc cgg cgg ggg cgc cac gag	96
Arg Arg Ala Ser Arg Ser Ser Gly Arg Ala Arg Arg Gly Arg His Glu	
20 25 30	
ccg ggg ctg ggg ggc ccg gcg gag cgc ggc gcg ggg gag gca cgg ctg	144
Pro Gly Leu Gly Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu	
35 40 45	
gaa gag gca gtc aat cgc tgg gtg ctc aag ttc tac ttc cac gag gcg	192
Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala	
50 55 60	
ctg cgg gcc ttt cgg ggt agc cgg tac ggg gac ttc aga cag atc cgg	240
Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg	
65 70 75 80	
gac atc atg cag gct ttg ctt gtc agg ccc ttg ggg aag gag cac acc	288
Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr	
85 90 95	
gtg tcc cga ttg ctg cgg gtt atg cag tgt ctg tcg cgg att gaa gaa	336
Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu	
100 105 110	
ggg gaa aat tta gac tgt tcc ttt gat atg gag gct gag ctc aca cca	384
Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro	
115 120 125	

ctg gaa tca gct atc aat gtg ctg gag atg att aaa acg gaa ttt aca	432
Leu Glu Ser Ala Ile Asn Val Leu Glu Met Ile Lys Thr Glu Phe Thr	
130 135 140	
ctg aca gaa gca gtg gtc gaa tcc agt aga aaa ctg gtc aag gaa gct	480
Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala	
145 150 155 160	
gct gtc att att tgt atc aaa aac aaa gaa ttt gaa aag gct tca aaa	528
Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys	
165 170 175	
att ttg aaa aaa cat atg tcc aag gac ccc aca act cag aag ctg aga	576
Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg	
180 185 190	
aat gat ctc ctg aat att att cga gaa aag aac ttg gcc cat cct gtt	624
Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val	
195 200 205	
atc cag aac ttt tca tat gag acc ttc cag cag aag atg ctg cgc ttc	672
Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe	
210 215 220	
ctg gag agc cac ctg gat gac gcc gag ccc tac ctc ctc acg atg gcc	720
Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala	
225 230 235 240	
aaa aag gct ttg aaa tct gag tcc gct gcc tca agt aca ggg aag gaa	768
Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu	
245 250 255	
gat aaa cag cca gca cca ggg cct gtg gaa aag cca ccc aga gaa ccc	816
Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro	
260 265 270	
gca agg cag cta cgg aat cct cca acc acc att gga atg atg act ctg	864
Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu	
275 280 285	
aaa gca gct ttc aag act ctg tct ggt gca cag gat tct gag gca gcc	912
Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala	
290 295 300	
ttt gca aaa ctg gac cag aag gat ctg gtt ctt cct act caa gct ctc	960
Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu	
305 310 315 320	
cca gca tca cca gcc ctc aaa aac aag aga ccc aga aaa gat gaa aac	1008
Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn	
325 330 335	
gaa agt tca gcc ccg gct gac ggt gag ggt ggc tcg gaa ctg cag ccc	1056
Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Gly Ser Glu Leu Gln Pro	
340 345 350	

aag aac aag cgc atg aca ata agc aga ttg gtc ttg gag gag gac agc	1104
Lys Asn Lys Arg Met Thr Ile Ser Arg Leu Val Leu Glu Glu Asp Ser	
355 360 365	
cag agt act gag ccc agc gca ggc ctc aac tcc tcc cag gag gcc gct	1152
Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala	
370 375 380	
tca gcg cca cca tcc aag c	